

# SEQUENCE LISTING

<110> Lowe, Keith S.  
Gordon-Kamm, William J.  
Klein, Theodore M.  
Rasco-Gaunt, Sonriza  
Cahoon, Rebecca E.  
Sun, Xifan  
Hoerster, George J.  
Gregory, Carolyn A.  
Nadimpalli, Ramgopal

<120> Transcriptional Activator Nucleic Acids,  
Polypeptides, and Methods of Use Thereof

<130> 0943

<150> 60/107,643

<151> 1998-11-09

<160> 23

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1173

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (69)...(902)

<400> 1

```
ccacgcgtcc gccaccacac cacgagcgcg cgataaccct agctagcttc aggtagtagc      60
gagagcca atg gac tcc agc agc ttc ctc cct gcc gcc ggc gcg gag aat      110
      Met Asp Ser Ser Phe Leu Pro Ala Ala Gly Ala Glu Asn
          1             5             10

ggc tcg gcg gcg ggc ggc gcc aac aat ggc ggc gct gct cag cag cat      158
Gly Ser Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His
      15             20             25             30

gcg gcg ccg gcg atc cgc gag cag gac cgg ctg atg ccg atc gcg aac      206
Ala Ala Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn
          35             40             45

gtg atc cgc atc atg cgg cgc gtg ctg ccg gcg cac gcc aag atc tcg      254
Val Ile Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser
          50             55             60

gac gac gcc aag gag acg atc cag gag tgc gtg tcg gag tac atc agc      302
Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser
          65             70             75

ttc atc acg ggg gag gcc aac gag cgg tgc cag cgg gag cag cgc aag      350
Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys
          80             85             90

acc atc acc gcc gag gac gtg ctg tgg gcc atg agc cgc ctc ggc ttc      398
```



20	25	30
Pro Ala Ile Arg Glu Gln Asp	Arg Leu Met Pro Ile Ala Asn Val Ile	
35	40	45
Arg Ile Met Arg Arg Val Leu Pro	Ala His Ala Lys Ile Ser Asp Asp	
50	55	60
Ala Lys Glu Thr Ile Gln Cys Val	Ser Glu Tyr Ile Ser Phe Ile	
65	70	75
Thr Gly Glu Ala Asn Glu Arg Cys	Gln Arg Glu Gln Arg Lys Thr Ile	
85	90	95
Thr Ala Glu Asp Val Leu Trp Ala	Met Ser Arg Leu Gly Phe Asp Asp	
100	105	110
Tyr Val Glu Pro Leu Gly Ala Tyr	Leu His Arg Tyr Arg Glu Phe Glu	
115	120	125
Gly Asp Ala Arg Gly Val Gly Leu	Val Pro Gly Ala Ala Pro Ser Arg	
130	135	140
Gly Gly Asp His His Pro His Ser	Met Ser Pro Ala Ala Met Leu Lys	
145	150	155
Ser Arg Gly Pro Val Ser Gly Ala	Ala Met Leu Pro His His His His	
165	170	175
His His Asp Met Gln Met His Ala	Ala Met Tyr Gly Gly Thr Ala Val	
180	185	190
Pro Pro Pro Ala Gly Pro Pro His	Gly Gly Phe Leu Met Pro His	
195	200	205
Pro Gln Gly Ser Ser His Tyr Leu	Pro Tyr Ala Tyr Glu Pro Thr Tyr	
210	215	220
Gly Gly Glu His Ala Met Ala Ala	Tyr Tyr Gly Gly Ala Ala Tyr Ala	
225	230	235
Pro Gly Asn Gly Gly Ser Gly Asp	Gly Ser Gly Ser Gly Gly Gly Gly	
245	250	255
Gly Ser Ala Ser His Thr Pro Gln	Gly Ser Gly Gly Leu Glu His Pro	
260	265	270
His Pro Phe Ala Tyr Lys		
275		

<210> 3  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 3  
 tagtagcgag agccaatgga

20

<210> 4  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 4  
 gccgggacag aatcacagta

20

<210> 5  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> primer

<400> 5  
tagtagcgag agccaatgga

20

<210> 6  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 6  
cccggcccta aaacaacaca

20

<210> 7  
<211> 481  
<212> DNA  
<213> Argemone mexicana

<220>  
<221> CDS  
<222> (44)...(481)  
  
<221> misc\_feature  
<222> (1)...(481)  
<223> n = A,T,C or G

<400> 7  
cgagagaaag agttggtgaa gaagaagaag aagttgaaaa gag atg gaa cgt ggt 55  
Met Glu Arg Gly  
1

ggt ggt ggt ggt ggt agt ggt ggt ggt ttc cat gga tat cag aaa ctc 103  
Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly Tyr Gln Lys Leu  
5 10 15 20

cca aaa tca aac tcc gct gga atg atg ctc tcg gag cta tcg aat aac 151  
Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu Leu Ser Asn Asn  
25 30 35

aac aac aat att gac gta aac tct aca tgt act gta cga gag caa gat 199  
Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val Arg Glu Gln Asp  
40 45 50

cga tac atg cca att gct aat gtg atc agg atc atg cgt aag gta ctt 247  
Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Val Leu  
55 60 65

cct act cat gcc aag atc tct gac gat gcc aaa gaa act atc caa gaa 295  
Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu  
70 75 80

tgt gtc tca gaa tac atc agt ttc atc aca agt gaa gcc aat gat cgt 343  
Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu Ala Asn Asp Arg  
85 90 95 100

tgc caa cgt gaa caa aga aag aca atc aca gct gaa gat gtt tta tgg 391  
Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp  
105 110 115

gcg atg agc aaa cta ggg ntt gat gag tac att gaa cct cta act ctt 439  
 Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu Pro Leu Thr Leu  
                   120                  125                  130

tac ctt caa cgt tat cgt gag ttt gaa ggt gna cgt tgg tca 481  
 Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg Trp Ser  
                   135                  140                  145

<210> 8  
 <211> 146  
 <212> PRT  
 <213> Argemone mexicana

<220>  
 <221> VARIANT  
 <222> (1)...(146)  
 <223> Xaa = Any Amino Acid

<400> 8  
 Met Glu Arg Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly  
   1                  5                  10                  15  
 Tyr Gln Lys Leu Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu  
                   20                  25                  30  
 Leu Ser Asn Asn Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val  
                   35                  40                  45  
 Arg Glu Gln Asp Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met  
                   50                  55                  60  
 Arg Lys Val Leu Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu  
                   65                  70                  75                  80  
 Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu  
                   85                  90                  95  
 Ala Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu  
                   100                  105                  110  
 Asp Val Leu Trp Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu  
                   115                  120                  125  
 Pro Leu Thr Leu Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg  
                   130                  135                  140  
 Trp Ser  
 145

<210> 9  
 <211> 942  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> CDS  
 <222> (3)...(722)

<400> 9  
 gc acg agc tct ctt ata atc aca cac aca cct acc tta ata gct atg 47  
   Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met  
   1                  5                  10                  15

gaa act gga ggc ttt cac ggc tac cgc aag ctc ccc aac acc acc gct 95  
 Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala  
                   20                  25                  30

ggg ttg aag ctg tca gtg tca gac atg aac atg agg cag cag gta gca 143  
 Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala  
                   35                  40                  45

tca tca gat cac agt gca gcc aca gga gag gag aac gaa tgc acg gtg Ser Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val	191
50 55 60	
agg gag caa gac agg ttc atg cca atc gcc aac gtg att agg atc atg Arg Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met	239
65 70 75	
cgc aag att ctc cct cca cac gca aaa atc tcg gac gat gca aaa gaa Arg Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu	287
80 85 90 95	
aca atc caa gag tgc gtg tct gag tac atc agc ttc atc aca ggt gag Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu	335
100 105 110	
gcg aac gag cgt tgc cag agg gag cag cgg aag acc ata acc gca gag Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu	383
115 120 125	
gac gtg ctt tgg gcc atg agc aag ctt gga ttc gac gac tac atc gaa Asp Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu	431
130 135 140	
ccg ttg acc atg tac ctt cac cgc tac cgt gaa ctt gag ggt gac cgc Pro Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg	479
145 150 155	
acc tct atg agg ggt gaa cca ctc ggg aag agg act gtg gaa tac gcc Thr Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala	527
160 165 170 175	
acg ctt ggt gtt gct act gct ttt gtc cct cca ccc tat cat cac cac Thr Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His	575
180 185 190	
aat ggg tac ttt ggt gct gcc atg ccc atg ggg act tac gtt agg gaa Asn Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu	623
195 200 205	
gcg cca cca aat aca gcc tcc tcc cat cac cac cac cac cac cac cac Ala Pro Pro Asn Thr Ala Ser Ser His His His His His His His His	671
210 215 220	
cac cat gct cgt gga atc tcc aat gct cat gaa cca aat gct cgc tcc His His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser	719
225 230 235	
ata taaaattata taattatgac taggattcag aacaagactt gatgatgatt Ile	772
240	
agcttaactc tcagtaattg gtgctagagt actactgttg ttgaggatac tttattttat	832
aattaagggc tgggaaggga gttagtatat tcctaatect aactatgtgc atctttaatt	892
tatgaaatca ctttgtttta acctttgatg aaaaaaaaaa aaaaaaaaaa	942

<210> 10  
 <211> 240  
 <212> PRT  
 <213> Glycine max

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

```
<220>  
<221> CDS  
<222> (58) ... (699)
```

7

[illegible]

```
<210> 12
<211> 214
<212> PRT
<213> Veronica mespilifolia
```

Met 1	Glu	Arg	Gly	Gly 5	Gly	Phe	His	Gly	Tyr 10	His	Arg	Leu	Pro	Ile 15	His
Pro	Thr	Ser	Gly 20	Ile	Gln	Gln	Ser	Asp 25	Met	Lys	Leu	Lys 30	Leu	Pro	Glu
Met	Thr	Asn 35	Asn	Asn	Ser	Ser	Thr 40	Asp	Asp	Asn	Glu	Cys 45	Thr	Val	Arg
Glu	Gln 50	Asp	Arg	Phe	Met	Pro 55	Ile	Ala	Asn	Val 60	Ile	Arg	Ile	Met	Arg
Lys 65	Ile	Leu	Pro	Pro	His 70	Ala	Lys	Ile	Ser 75	Asp	Asp	Ala	Lys	Glu 80	Thr
Ile	Gln	Glu	Cys	Val 85	Ser	Glu	Tyr	Ile	Ser 90	Phe	Val	Thr	Gly 95	Glu	Ala



Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp  
                   100                  105                  110  
 Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro  
                   115                  120                  125  
 Leu Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg  
                   130                  135                  140  
 Gly Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro  
 145                  150                  155                  160  
 Gly His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His  
                   165                  170                  175  
 His Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp  
                   180                  185                  190  
 Pro Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro  
                   195                  200                  205  
 Tyr Ala Gln Cys Lys Glu  
 210

<210> 13  
 <211> 763  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (1)...(480)

<400> 13

gca cga ggc aag acc gtc acc tcc gag gac atc gtg tgg gcc atg agc	48
Ala Arg Gly Lys Thr Val Thr Ser Glu Asp Ile Val Trp Ala Met Ser	
1                  5                  10                  15	
cgc ctc ggc ttc gac gac tac gtc gcg ccc ctc ggc gcc ttc ctc cag	96
Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln	
20                  25                  30	
cgc atg cgc gac gac agc gac cac ggc ggt gaa gag cgc ggc ggc cct	144
Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro	
35                  40                  45	
gca ggg cgt ggt ggc tcg cgc cgc ggc tcg tcg tcc ttg ccg ctc cac	192
Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His	
50                  55                  60	
tgc ccg cag cag atg cac cac ctg cac cca gcc gtc tgc cgg cgt ccg	240
Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro	
65                  70                  75                  80	
cac cag agc gtg tcg cct gct gca gga tac gcc gtc cgg ccc gtt ccc	288
His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro	
85                  90                  95	
cgc ccg atg cca gcc cgt ggg tac cgc atg cag ggc gga gac cac cgc	336
Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg	
100                  105                  110	
agc gtg ggc ggc gtg gct ccc tgc agc tac gga ggg gcg ctc gtc cag	384
Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln	
115                  120                  125	
gcc ggt gga acc caa cac gtt gtt gga ttc cac gac gac gag gca agc	432
Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser	
130                  135                  140	

tct tcg agt gaa aat ccg ccg ccg gag ggg cgt gcc gct ggc tcg aac 480  
 Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn  
 145 150 155 160

tagcctagct tctcagttcc cctgtgtacaa taagaggggc ggtcgcggcg ccgcgccgcg 540  
 cccttgggtt gggccgggcg ctatgctgca gtttggtttg taaactaacg agcctagggt 600  
 agctggtgca cgcgcgccac ctgcgccgac gtcgccgtcg tcgtcgcat ggacttaacc 660  
 ggcgggccct gttgttattt ctcaagtttg tagccaacgc actgttcggt gcgttcata 720  
 atttaattta ccatgttgct ctcgaaaaaa aaaaaaaaaa aaa 763

<210> 14  
 <211> 160  
 <212> PRT  
 <213> Zea mays

<400> 14  
 Ala Arg Gly Lys Thr Val Thr Ser Glu Asp Ile Val Trp Ala Met Ser  
 1 5 10 15  
 Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln  
 20 25 30  
 Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro  
 35 40 45  
 Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His  
 50 55 60  
 Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro  
 65 70 75 80  
 His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro  
 85 90 95  
 Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg  
 100 105 110  
 Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln  
 115 120 125  
 Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser  
 130 135 140  
 Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn  
 145 150 155 160

<210> 15  
 <211> 622  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (3)...(622)  
 <221> misc\_feature  
 <222> (1)...(622)  
 <223> n = A,T,C or G

<400> 15  
 gc atg aat aat ccc caa aac cct aaa gcc agt gct cct tgc acc ttg 47  
 Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu  
 1 5 10 15

cca ccg gag ctt ccc aaa gaa gca gtg gcg acc gac gaa gca ccg ccg 95  
 Pro Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro  
 20 25 30

cca atg ggc aac aac aac aac acg gaa tcg gcg acg gcg acg atg gtc 143  
 Pro Met Gly Asn Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val

45



Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu  
130 135 140

cac cgc tac cgt gag ctg gag ggt gac cgc acc tct atg agg ggt gaa 479  
 His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu  
 145 150 155

cgc ctc ggg aag agg act gtg gaa tat gcc acg ctt gct act gct ttt 527  
Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe  
160 165 170 175

gtg ccg cca ccc ttt cat cac cac aat ggc tac ttt ggt gct gcc atg 575  
Val Pro Pro Pro Phe His His His Asn Gly Tyr Phe Gly Ala Ala Met  
180 185 190

ccc atg ggg act tac gtt agg gaa acg cca cca aat gct gcg tca tct 623  
Pro Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser  
195 200 205

```

cat cac cat cat gga atc tcc aat gct cat gaa cca aat gct cgc tcc      671
His His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser
          210                      215                      220

```

ata	taa	aat	taa	tga	aga	gta	ctg	ttc	agt	agg	aga	aca	aga	ctt	ctt	719
Ile	*	Asn	*	*	Arg	Val	Leu	Phe	Ser	Arg	Arg	Thr	Arg	Leu	Leu	
		225							230					235		

gga ctt gat tag ctt aac tct cag tga ttg gtg tta gag tac tgt tgt 767  
Gly Leu Asp \* Leu Asn Ser Gln \* Leu Val Leu Glu Tyr Cys Cys  
240 245 250

tga gga tgg tta att tta taa tta agg gct ggg aat tgg gga gtt agt 815  
\* Gly Trp Leu Ile Leu \* Leu Arg Ala Gly Asn Trp Gly Val Ser  
255 260

```
ata tat tcc taa tcc taa tta tgt gca tct tta att tat gga ata act      863
Ile Tyr Ser * Ser * Leu Cys Ala Ser Leu Ile Tyr Gly Ile Thr
265                               270                       275
```

ttg ttt ttt gtt tta act tct gat aat ttg gat ttt ctg atg ttt aat 911  
Leu Phe Phe Val Leu Thr Ser Asp Asn Leu Asp Phe Leu Met Phe Asn  
280 285 290

gtg gtt ttg tct atc cct tat taa cag tgc caa gct taa ggt ttt agc 959  
Val Val Leu Ser Ile Pro Tyr \* Gln Cys Gln Ala \* Gly Phe Ser  
295 300 305

cat gct cca aaa tgg aat act tgt act gtt atg ttg ttc tgg tag tga 1007  
His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu Phe Trp \* \*  
310 315 320

tgg	tga	tga	aac	ctg	caa	gtt	atg	ttt	atg	tat	aaa	gcc	act	att	gat	1055
Trp	*	*	Asn	Leu	Gln	Val	Met	Phe	Met	Tyr	Lys	Ala	Thr	Ile	Asp	
				325					330					335		

caa aat tag aga aat tat cat tta ata agt atc ctc cca tgt taa ttt 1103  
Gln Asn \* Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys \* Phe  
340 345 350

```
taa aaa aaa aaa aaa aaa                                     1121
 *   Lys Lys Lys Lys Lys
                               355
```

<210> 18  
 <211> 355  
 <212> PRT  
 <213> Glycine max

<400> 18

Thr	Arg	Glu	Thr	Gly	Gly	Phe	His	Gly	Tyr	Arg	Lys	Leu	Pro	Asn	Thr
1				5				10						15	
Thr	Ser	Gly	Leu	Lys	Leu	Ser	Val	Ser	Asp	Met	Asn	Met	Asn	Met	Arg
		20						25					30		
Gln	Gln	Gln	Val	Ala	Ser	Ser	Asp	Gln	Asn	Cys	Ser	Asn	His	Ser	Ala
		35					40					45			
Ala	Gly	Glu	Glu	Asn	Glu	Cys	Thr	Val	Arg	Glu	Gln	Asp	Arg	Phe	Met
	50					55					60				
Pro	Ile	Ala	Asn	Val	Ile	Arg	Ile	Met	Arg	Lys	Ile	Leu	Pro	Pro	His
65					70					75					80
Ala	Lys	Ile	Ser	Asp	Asp	Ala	Lys	Glu	Thr	Ile	Gln	Glu	Cys	Val	Ser
			85						90					95	
Glu	Tyr	Ile	Ser	Phe	Ile	Thr	Gly	Glu	Ala	Asn	Glu	Arg	Cys	Gln	Arg
			100					105						110	
Glu	Gln	Arg	Lys	Thr	Ile	Thr	Ala	Glu	Asp	Val	Leu	Trp	Ala	Met	Ser
		115					120						125		
Lys	Leu	Gly	Phe	Asp	Asp	Tyr	Ile	Glu	Pro	Leu	Thr	Met	Tyr	Leu	His
	130					135						140			
Arg	Tyr	Arg	Glu	Leu	Glu	Gly	Asp	Arg	Thr	Ser	Met	Arg	Gly	Glu	Pro
145					150						155				160
Leu	Gly	Lys	Arg	Thr	Val	Glu	Tyr	Ala	Thr	Leu	Ala	Thr	Ala	Phe	Val
			165						170					175	
Pro	Pro	Pro	Phe	His	His	His	Asn	Gly	Tyr	Phe	Gly	Ala	Ala	Met	Pro
			180					185						190	
Met	Gly	Thr	Tyr	Val	Arg	Glu	Thr	Pro	Pro	Asn	Ala	Ala	Ser	Ser	His
		195					200					205			
His	His	His	Gly	Ile	Ser	Asn	Ala	His	Glu	Pro	Asn	Ala	Arg	Ser	Ile
		210				215						220			
Asn	Arg	Val	Leu	Phe	Ser	Arg	Arg	Thr	Arg	Leu	Leu	Gly	Leu	Asp	Leu
225					230					235					240
Asn	Ser	Gln	Leu	Val	Leu	Glu	Tyr	Cys	Cys	Gly	Trp	Leu	Ile	Leu	Leu
			245						250					255	
Arg	Ala	Gly	Asn	Trp	Gly	Val	Ser	Ile	Tyr	Ser	Ser	Leu	Cys	Ala	Ser
			260					265						270	
Leu	Ile	Tyr	Gly	Ile	Thr	Leu	Phe	Phe	Val	Leu	Thr	Ser	Asp	Asn	Leu
		275					280						285		
Asp	Phe	Leu	Met	Phe	Asn	Val	Val	Leu	Ser	Ile	Pro	Tyr	Gln	Cys	Gln
		290				295					300				
Ala	Gly	Phe	Ser	His	Ala	Pro	Lys	Trp	Asn	Thr	Cys	Thr	Val	Met	Leu
305					310					315					320
Phe	Trp	Trp	Asn	Leu	Gln	Val	Met	Phe	Met	Tyr	Lys	Ala	Thr	Ile	Asp
			325						330					335	
Gln	Asn	Arg	Asn	Tyr	His	Leu	Ile	Ser	Ile	Leu	Pro	Cys	Phe	Lys	Lys
			340					345					350		
Lys	Lys	Lys													
			355												

<210> 19  
 <211> 796  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> CDS

<222> (1) ... (513)

<400> 19

gca cga gca atg gcg gga gtg agg gaa cag gac cag tac atg ccg ata 48  
Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile  
1 5 10 15

gcg aac gtg ata agg atc atg cgt cgg att ctg cca gcg cac gcg aag 96  
Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys  
20 25 30

atc tca gac gac gcg aag gag acg atc cag gag tgc gtg tct gag tac 144  
Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr  
35 40 45

atc agt ttc atc acg gcg gag gcg aac gag cgg tgc cag cgg gag cag 192  
Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln  
50 55 60

cgg aag acg gtg acc gca gag gat gtg ttg tgg gcg atg gag aag ctt 240  
Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu  
65 70 75 80

ggc ttt gac aac tac gct cac cct ctc tct ctt tac ctt cac cgc tac 288  
Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr  
85 90 95

cgc gag agt gaa gga gaa cct gct tct gtc aga cgc gct tct tct gca 336  
Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala  
100 105 110

atg ggg atc aat aat aat atg gtg cac cca cct tat att aat tct cat 384  
Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His  
115 120 125

ggc ttt gga atg ttt gat ttt gac cca tca tcg caa ggg ttt tac agg 432  
Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg  
130 135 140

gac gat cat aac gct gct tct gga tct ggt ggt ttt gtt gcg cct ttt 480  
Asp Asp His Asn Ala Ala Ser Gly Ser Gly Gly Phe Val Ala Pro Phe  
145 150 155 160

gat cct tat gct aac atc aaa cgt gat gcc ctg tgatcatgta agaacaacaa 533  
Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu  
165 170

ctagtgcattg ctgcttttttc acttggttag ttatattcaa gcacaagcac atgcaggtgc 593  
agctgcaact atttagcttc atctacaaat ctttttttct ctcttcttct catgctttaa 653  
ttatttagag acaatacttg ttattcattg ttatgctcaa ttgctagctt ctattcatcg 713  
tcgactgtct gtattgttga tggttcattac agtaacagat aagatggtaa ctgctttact 773  
acttcaaaaaa aaaaaaaaaa aaa 796

<210> 20

<211> 171

<212> PRT

<213> Glycine max

<400> 20

Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile  
1 5 10 15  
Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys

			20					25					30			
Ile	Ser	Asp	Asp	Ala	Lys	Glu	Thr	Ile	Gln	Glu	Cys	Val	Ser	Glu	Tyr	
		35					40					45				
Ile	Ser	Phe	Ile	Thr	Ala	Glu	Ala	Asn	Glu	Arg	Cys	Gln	Arg	Glu	Gln	
	50					55					60					
Arg	Lys	Thr	Val	Thr	Ala	Glu	Asp	Val	Leu	Trp	Ala	Met	Glu	Lys	Leu	
65					70				75						80	
Gly	Phe	Asp	Asn	Tyr	Ala	His	Pro	Leu	Ser	Leu	Tyr	Leu	His	Arg	Tyr	
				85				90						95		
Arg	Glu	Ser	Glu	Gly	Glu	Pro	Ala	Ser	Val	Arg	Arg	Ala	Ser	Ser	Ala	
			100					105					110			
Met	Gly	Ile	Asn	Asn	Asn	Met	Val	His	Pro	Pro	Tyr	Ile	Asn	Ser	His	
		115					120					125				
Gly	Phe	Gly	Met	Phe	Asp	Phe	Asp	Pro	Ser	Ser	Gln	Gly	Phe	Tyr	Arg	
	130					135					140					
Asp	Asp	His	Asn	Ala	Ala	Ser	Gly	Ser	Gly	Gly	Phe	Val	Ala	Pro	Phe	
145					150					155					160	
Asp	Pro	Tyr	Ala	Asn	Ile	Lys	Arg	Asp	Ala	Leu						
				165				170								

```
<210> 21
<211> 1098
<212> DNA
<213> Triticum aestivum
```

```
<220>
<221> CDS
<222> (55) ... (894)
```

<400> 21																57
gcacgagcaa	gtgcgagtgc	gactacctgc		attgcacctt		ggctagccct		agac		atg		Met		1		
gag	aac	gac	ggc	gtc	ccc	aac	gga	cca	gcg	gcg	ccg	gca	cct	acc	cag	105
Glu	Asn	Asp	Gly	Val	Pro	Asn	Gly	Pro	Ala	Ala	Pro	Ala	Pro	Thr	Gln	
			5					10					15			
ggg	acg	ccg	gtg	gtg	cgg	gag	cag	gac	cgg	ctg	atg	ccg	atc	gcg	aac	153
Gly	Thr	Pro	Val	Val	Arg	Glu	Gln	Asp	Arg	Leu	Met	Pro	Ile	Ala	Asn	
			20					25					30			
gtg	atc	cgc	atc	atg	cgc	cgt	gcg	ctc	cct	gcc	cac	gcc	aag	atc	tcc	201
Val	Ile	Arg	Ile	Met	Arg	Arg	Ala	Leu	Pro	Ala	His	Ala	Lys	Ile	Ser	
			35					40					45			
gac	gac	gcc	aag	gag	gcg	att	cag	gaa	tgc	gtg	tcc	gag	ttc	atc	agc	249
Asp	Asp	Ala	Lys	Glu	Ala	Ile	Gln	Glu	Cys	Val	Ser	Glu	Phe	Ile	Ser	
			50					55					60		65	
ttc	gtc	acc	ggc	gag	gcc	aac	gaa	cgg	tgc	cgc	atg	cag	cac	cgc	aag	297
Phe	Val	Thr	Gly	Glu	Ala	Asn	Glu	Arg	Cys	Arg	Met	Gln	His	Arg	Lys	
			70					75					80			
acc	gtc	aac	gcc	gaa	gac	atc	gtg	tgg	gcc	cta	aac	cgc	ctc	ggc	ttc	345
Thr	Val	Asn	Ala	Glu	Asp	Ile	Val	Trp	Ala	Leu	Asn	Arg	Leu	Gly	Phe	
			85					90					95			
gac	gac	tac	gtc	gtg	ccc	ctc	agc	gtc	ttc	ctg	cac	cgc	atg	cgc	gac	393
Asp	Asp	Tyr	Val	Val	Pro	Leu	Ser	Val	Phe	Leu	His	Arg	Met	Arg	Asp	
			100					105					110			



ccc gag gcg ggg aca ggt ggt gcc gct gca ggc gac agc cgc gcc gtg 441  
 Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala Val  
 115 120 125  
 acg agt gcg cct ccc cgc gcg gcc ccg ccc gtg atc cac gcc gtg ccg 489  
 Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val Pro  
 130 135 140 145  
 ctg cag gct cag cgc ccg atg tac gcg ccc ccg gct ccg ttg cag gtt 537  
 Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln Val  
 150 155 160  
 gag aat cag atg cag cgg cct gtg tac gct ccc ccg gct ccg gtg cag 585  
 Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val Gln  
 165 170 175  
 gtt cag atg cag cgg gcc atc tat ggg ccc cgg gct cca gtg cac ggg 633  
 Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His Gly  
 180 185 190  
 tac gcc gtc gga atg gcg ccc gtg cgg gcc aac gtc gcc ggg cag tac 681  
 Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln Tyr  
 195 200 205  
 cag gtg ttc gcc gga gag ggt gtc atg gcc cag caa tac tac ggg tac 729  
 Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly Tyr  
 210 215 220 225  
 ggg tac gag gaa gga gcg tac gcc gca ggt agc agc aac gga gga gcc 777  
 Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly Ala  
 230 235 240  
 gcc att gcc gac gag gag agc tcg tcc aac gcc gtg ccg gca ccg ggg 825  
 Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro Gly  
 245 250 255  
 gag gcc atg ggg gag cca gag cca gag cca gca gca gaa gaa tcg cat 873  
 Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser His  
 260 265 270  
 gac aag ccc gtc caa tct gcc tagtcgcgtg cgcggcgcgc gttagcttct 924  
 Asp Lys Pro Val Gln Ser Gly  
 275 280  
 gcgtcctgtg tactgtaata atttgccgtg tcgatccggc catggtttgt gtgtgcgtag 984  
 tgcttatcta atgtgggctt gtcctctagt aattcatgta ttgcttatct aatgtggact 1044  
 tgctctctag taattcatgt actctttgct gttgaaaaaa aaaaaaaaaa aaaa 1098

<210> 22  
 <211> 280  
 <212> PRT  
 <213> Triticum aestivum

<400> 22  
 Met Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr  
 1 5 10 15  
 Gln Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala  
 20 25 30  
 Asn Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile  
 35 40 45  
 Ser Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile  
 50 55 60

Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg  
 65 70 75 80  
 Lys Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly  
 85 90 95  
 Phe Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg  
 100 105 110  
 Asp Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala  
 115 120 125  
 Val Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val  
 130 135 140  
 Pro Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln  
 145 150 155 160  
 Val Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val  
 165 170 175  
 Gln Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His  
 180 185 190  
 Gly Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln  
 195 200 205  
 Tyr Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly  
 210 215 220  
 Tyr Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly  
 225 230 235 240  
 Ala Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro  
 245 250 255  
 Gly Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser  
 260 265 270  
 His Asp Lys Pro Val Gln Ser Gly  
 275 280

<210> 23  
 <211> 65  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> LEC1 consensus protein sequence  
  
 <221> VARIANT  
 <222> (1)...(65)  
 <223> Xaa = Any Amino Acid

<400> 23  
 Arg Glu Gln Asp Xaa Xaa Met Pro Ile Ala Asn Val Ile Arg Ile Met  
 1 5 10 15  
 Arg Xaa Xaa Leu Pro Xaa His Ala Lys Ile Ser Asp Asp Ala Lys Glu  
 20 25 30  
 Xaa Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Xaa Thr Xaa Glu  
 35 40 45  
 Ala Asn Xaa Arg Cys Xaa Xaa Xaa Arg Lys Thr Xaa Xaa Xaa Glu  
 50 55 60  
 Xaa  
 65